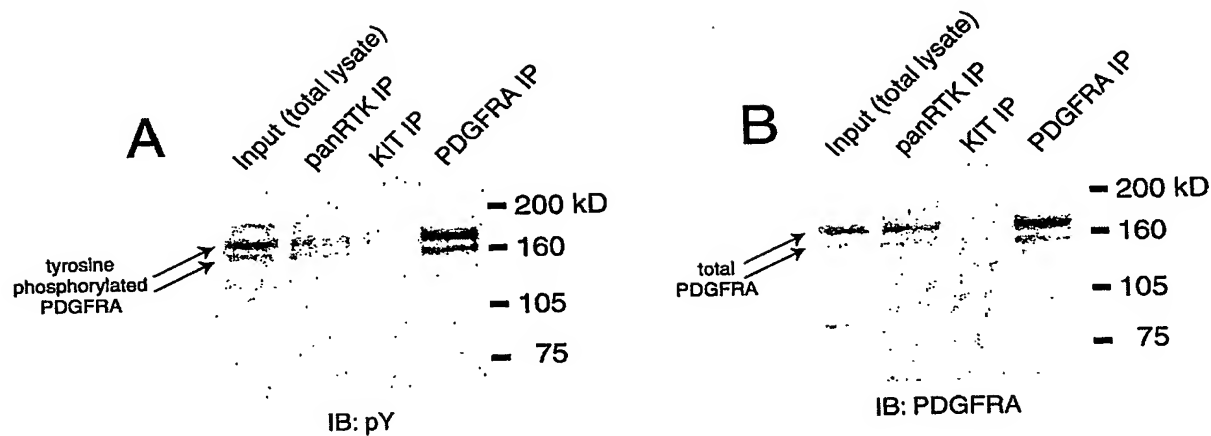


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FIGURE 1



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FIGURE 2A

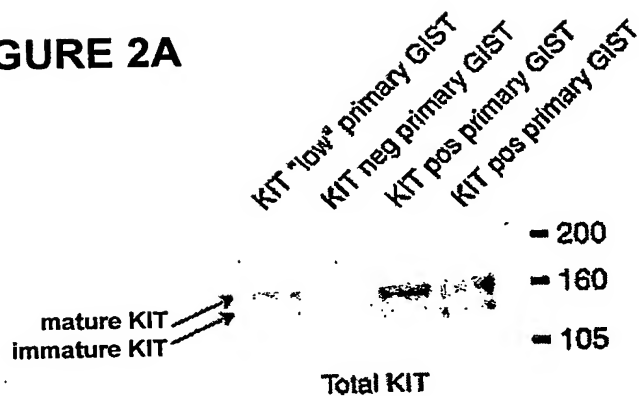


FIGURE 2B

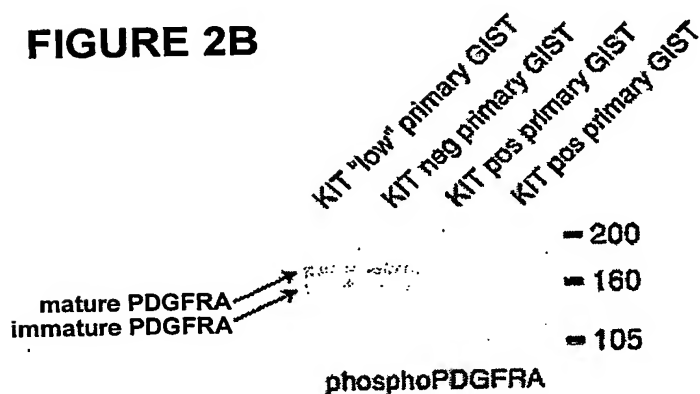


FIGURE 2C

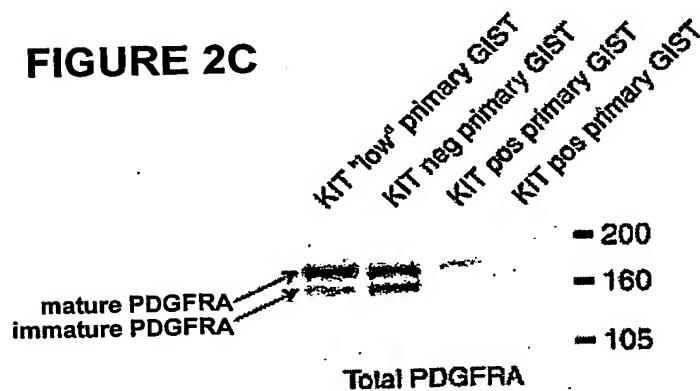


FIGURE 3

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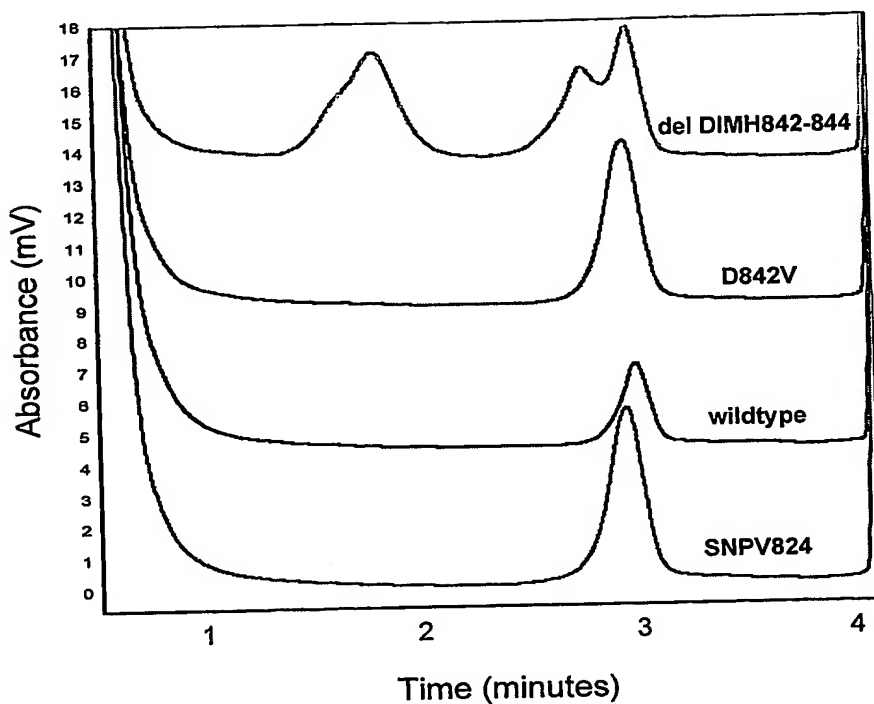
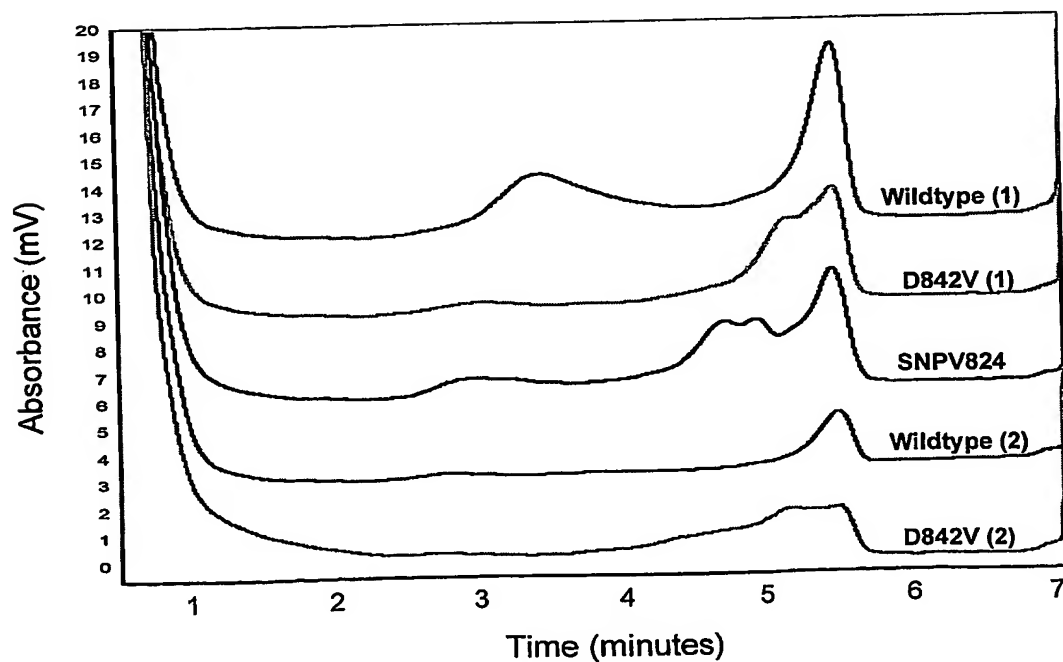


FIGURE 4



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FIGURE 5

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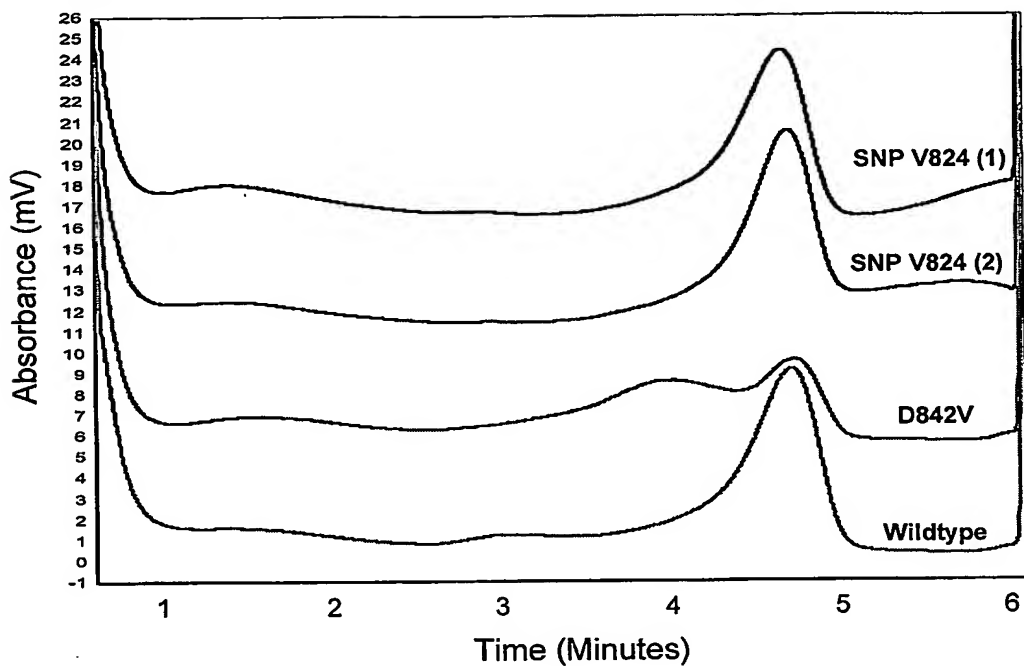
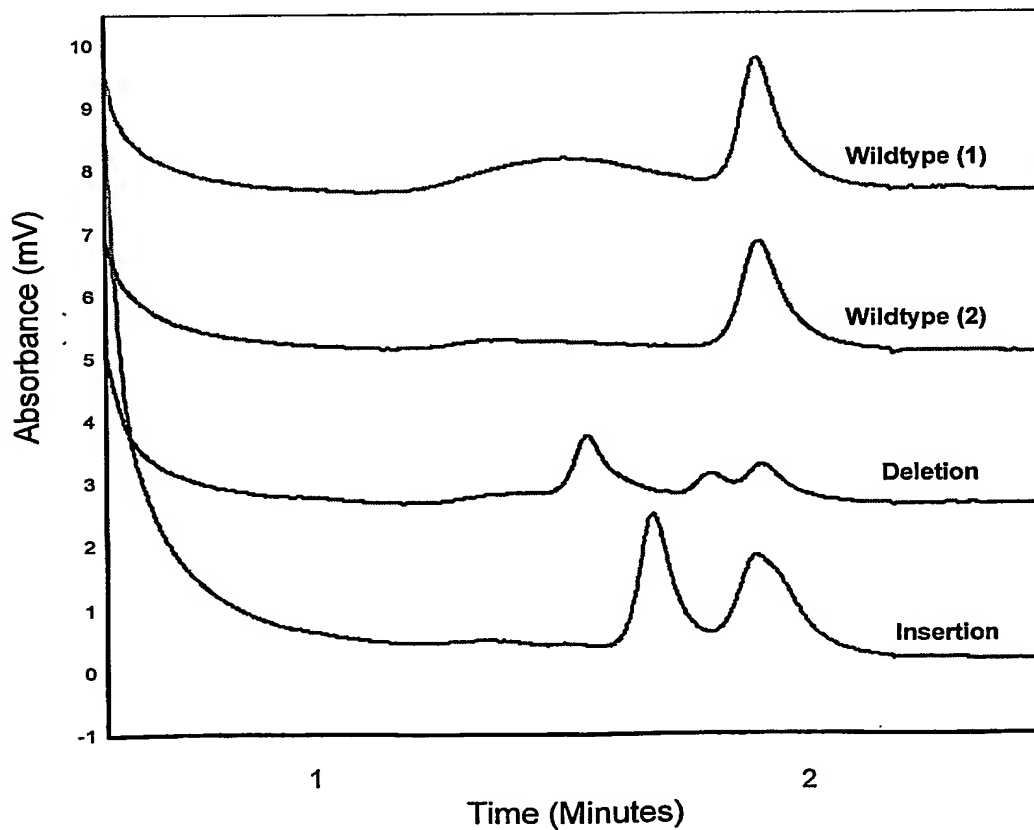


FIGURE 6



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FIGURE 7A

181551 GCTTTCTCTC TGTTGGGAGT GGGTGGAGTG AGAACCTGGG AGAAGGCCAG
CGAAAGAGAG ACAACCCTCA CCCACCTCAC TCTTGGACCC TCTTCCGGTC
A F S L L G V G G V R T W E K A S Frame 3

PDGFrA 181534F

181601 CCCTTTATAT CCAGGCAGAC AGCTCCAAGT GCCACCATCG ATCAGCCAGT
GGGAAATATA GGTCCGTCTG TCGAGGTTCA CCGTGGTACC TAGTCGGTCA
P L Y P G R Q L Q V P P W I S Q S Frame 3

PDGFrA 181640F PDGFrA 181671F

181651 CTTGCAGGGG TGATGCTATT CAGCTACAGA TGGCTTGATC CTGAGTCATT
GAACGTCCCC ACTACGATAA GTCGATGTCT ACCGAAGTAG GACTCAGTAA
C R G D A I Q L Q M A * S * V I Frame 3

181701 TCTTCCTTTT CCATGCAGTG TGTCCACCGT GATCTGGCTG CTCGCAACGT
AGAAGGAAAA GGTACGTCAC ACAGGTGGCA CTAGACCGAC GAGCGTTGCA
S S F S M Q C V H R D L A A R N V Frame 3

PDGFrA 181752F (SNP Exclusion)

181751 CCTCCTGGCA CAAGGAAAAA TTGTGAAGAT CTGTGACTTT GGCCTGGCCA
GGAGGACCGT GTTCCTTTTT AACACTTCTA GACACTGAAA CCGGACCGGT
L L A Q G K I V K I C D F G L A R Frame 3

181801 GAGACATCAT GCATGATTCT AACTATGTGT CGAAAGGCAG TGTACGTCCT
CTCTGTAGTA CGTACTAAGC TTGATACACA GCTTTCCGTC ACATGCAGGA
D I M H D S N Y V S K G S V R P Frame 3

PDGFrA 181862R PDGFrA 181874R

181851 CACTTCCCTC ACTGGTCAGG CTCATCCTCC TTCACTTTAA TCTCTAAAGT
GTGAAGGGAG TGACCAGTCC GAGTAGGAGG AAGTGAAATT AGAGATTTC
H F P H W S G S S S F T L I S K V Frame 3

181901 CAGGTGTTGC TTCTAGAGAT TCGGTGCCTG TTTTAAAAA CATCAATAGA
GTCCACAACG AAGATCTCTA AGCCACGGAC AAAAAATTTT GTAGTTATCT
R C C F * R F G A C F L K H Q * I Frame 3

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FIGURE 7B

170551 AAGCATAGCA ACCTAGTTCA GTGCTTGGCA CAGAGAAGGA GCTCAGCAAT
TTCGTATCGT TGGATCAAGT CACGAACCGT GTCTCTTCCT CGAGTCGTTA
K H S N L V Q C L A Q R R S S A I Frame 1

PDGFrA 170636F

170601 TACATGTGGA GTGAACGTTG TTGGACTCTA CTGTGTCCAG TCACTGTGCT
ATGTACACCT CACTTGCAAC AACCTGAGAT GACACAGGTC AGTGACACGA
T C G V N V V G L Y C V Q S L C C Frame 1

PDGFrA 170658F

170651 GCTTCAGTGA AGCTCTGGTG CACTGGGACT TTGGTAATTC ACCAGTTACC
CGAAGTCAC TCGAGACCAC GTGACCCTGA AACCATTAAAG TGGTCAATGG
F S E A L V H W D F G N S P V T Frame 1

170701 TGTCCTGGTC ATTTATAGAA ACCGAGGTAT GAAATTCGCT GGAGGGTCAT
ACAGGACCAG TAAATATCTT TGGCTCCATA CTTTAAGCGA CCTCCAGTA
C P G H L * K P R Y E I R W R V I Frame 1 Exon 12

170751 TGAATCAATC AGCCCAGATG GACATGAATA TATTTATGTG GACCCGATGC
ACTTAGTTAG TCGGGTCTAC CTGTACTTAT ATAAATACAC CTGGGCTACG
E S I S P D G H E Y I Y V D P M Q Frame 1

170801 AGCTGCCTTA TGA CTCAAGA TGGGAGTTTC CAAGAGATGG ACTAGTGCTT
TCGACGGAAT ACTGAGTTCT ACCCTCAAAG GTTCTCTACC TGATCAGAA
L P Y D S R W E F P R D G L V L Frame 1

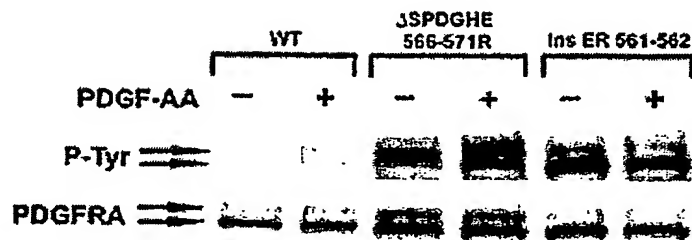
PDGFrA 170866R PDGFrA 170894R

170851 GGTAAGTTCC ATGGGGTAAC CTCCCAAGAC TCCCTTTTCC CTTGCACACA
CCATTCAAGG TACCCCATTG GAGGGTTCTG AGGGAAAAGG GAACGTGTGT
G K F H G V T S Q D S L F P C T Q Frame 1

170901 ACTTTACAAT TTATAGGCCT TGGCAGAATA GAGATCTGAG CTTGTGCTTA
TGAAATGTTA AATATCCGGA ACCGTCTTAT CTCTAGACTC GAACACGAAT
L Y N L * A L A E * R S E L V L S Frame 1

FIGURE 8

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Exon 12



Exon 18

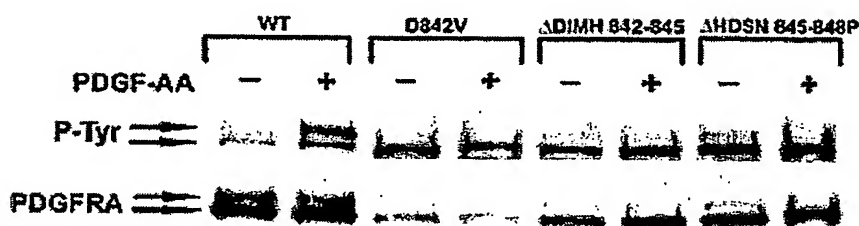


FIGURE 9

